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86128

Fr m: Bunner, Bridget
Sent: Thursday, February 06, 2003 11:54 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like a sequence search performed for case 09/762,594:

1. the nucleic acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

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Point of Contact:
Susan Hanley
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Searcher: _____
Phone: _____
Location: _____
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Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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(GEORGE) UNIV GEORGETOWN MEDICAL CENT.

Papadopoulos V, Li H:

WPT: 2000-224278/19.

P-PSDB; AAY67500;

Novel peripheral-type benzodiazepine receptor associated proteins used for the regulation of the peripheral-type benzodiazepine receptor -

Claim 3: Page 68: 71pp: English.

The invention provides isolated peripheral-type benzodiazepine receptor (PBR) associated proteins (PAPs) and nucleic acids encoding the PAP proteins. The PAP polynucleotides are a source of primers and probes for detection, isolation and amplification. PAP ligands or substrates or antibodies can be labeled and used to detect PAPs, in the diagnosis and prognosis of disease associated with increased cell proliferation, such as cancer, or reduced cell death. The diagnostic methods of the invention can be predictive of diseases involving PBR including gallstones, atherosclerosis, Niemann-Pick C, Sittosterolemia, Dystrophy, tumor proliferation, Schnyder's corneal crystalline dystrophy, brain disorders including Alzheimer's disease, cholesterol metabolism, Tellurium toxicity, Smith-Lemli-Opitz syndrome, myelinization, developmental abnormalities, demyelination, Charcot-Marie tooth disease, Pelizaeus-Werzbacher disease, Multiple sclerosis, and SMA. The methods may also be useful in prophylactic treatments, or in screening for compounds effective in prophylactic treatment. The PAPs may be used to identify inhibitors or activators which allows the identification of drugs or agents which modulate PBR activity. Inhibitors of PAP may be used in the treatment or amelioration of conditions such as stress and stroke, cancer, neurodegenerative disorders, developmental disorders, infertility and immune disorders. The present sequence represents a cDNA encoding a PAP7 polypeptide.

Sequence 1459 BP: 455 A: 298 C: 403 G: 303 T: 0 other:

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Query Match      100.0%; Score 1459; DB 21; Length 1459;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 GAATTTCGGCGCGCGTTCGACCTAAAGTTGAGTTGTTCACTGTAGTGACCCGTTGAAGGT 60

61 AGTTTATA TTTTAA AATCAA CTTTCA TTGTGCA AACTGCTA AAGATGCC AAGCCCTTCA 120

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181 A T A T A A C C C A G A C A C G T C C C C T G A G G T T G G A T T C T T T G A T G T T G G G G A A T G A T A G G A G 240

241 GAGAGAA TGGCAGCTCTGGGAAACATGTCCAAGGAGGATGCCCATGGTAGAGTTTGTGAA 300

301 GCTTCTAAATAAGTGTGTCTCTCTCTCGGCATATGTTGCGTCCACAGAAATAGAGAA 360

[illegible]

361 GGAAGAAGAGAAAGAAGAAAGCGGAGGAGCGAAGCGTGAAGAGGAAGA 420

[illegible]

421 ACGAGAGCGGCTGCAAAAGGAAGAAGAGACCGAAGCAGAGGAGACCGGCTGAG 480

RESULT 2

AAK52051

ID AAK52051 standard; cDNA; 3399 BP.

XX

Qy	1357	GAGTCCAAAGTCGCTACACAGAGCTATTATTACTAGATAGAGCTGCTGTCCAAAGT	1416		
Db	1557	CGCGTCAAAATCAGCTACACAGAGCTATTATTACTAGATAAAATGTTGTACAAAGT	1616		
Qy	1417	CCGAGTCCAGGGTTGAGCACACATCAGCTTTAAATTT	1454		
Db	1617	CTGGAGTCTAGGGTTGGCAGAGATGACATTTAAATTT	1654		
RESULT 3					
AAZ87207	standard; cDNA; 1481 BP.				
XX	AAZ87207;				
XX	08-MAY-2000	(first entry)			
XX	Human NTAP cDNA clone 998868.				
DE	Neurotransmission-associated protein; NTAP;				
KW	benzodiazepine receptor-associated protein; neurological disease;				
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease;				
KW	cerebral neoplasm; multiple sclerosis; drug screening; gene therapy;				
KW	antagonist; cancer; AIDS; asthma; Crohn's disease; osteoporosis; ss.				
XX	OS	Homo sapiens.			
XX	Key	Location/Qualifiers			
FT	CDS	146..1372			
FT	/*tag= a				
FT	/product= "Human neurotransmission-associated protein				
XX	(NTAP) 998868"				
XX	W0200001821-A2.				
PD	13-JAN-2000.				
XX	02-JUL-1999;	99WO-US15121.			
XX	02-JUL-1998;	98US-0091677.			
XX	(INCY-) INCYTE PHARM INC.				
XX	Lal P,	Tang YT, Yue H, Corley NC, Guegler KJ, Gorgone GA;			
PI	Baughn MR,	Patterson C;			
XX	WPI: 2000-160770/14.				
DR	P-PSDB; AAY77123.				
XX	New human neurotransmission associated proteins, useful for treatment,				
PT	prevention and diagnosis of neurological disease, e.g. Alzheimer's				
PT	disease, and antagonists for treating cancer or immune disorders -				
XX	Claim 7; Page 65; 67pp; English.				
XX	Sequences AAZ87205-Z87210 represent cDNAs encoding six human				
CC	neurotransmission-associated proteins (NTAPs, AAY77121-Y77126). The				
CC	present sequence, clone 998868, encodes a benzodiazepine				
CC	receptor-associated protein, and was produced by extension of cDNA				
CC	fragments isolated from a human kidney tumour cDNA library. The NTAPs are				
CC	used for treatment or prevention of neurological diseases (e.g.,				
CC	Alzheimer's, Parkinson's or Huntington's diseases, cerebral neoplasms, or				
CC	multiple sclerosis). They can also be used to raise specific antibodies				
CC	and to screen for specific binding agents (potential agonists and				
CC	antagonists). NTAP-encoding nucleic acids are useful for recombinant				
CC	production of NTAPs, and as a source of therapeutic antagonists				
CC	(antisense, triplex-forming or ribozyme molecules). The nucleic acids may				
CC	also be used as a source of probes and primers for diagnosis or				
CC	monitoring of NTAP expression in hybridisation/amplification tests, for				
CC	chromosome mapping and for identifying related sequences, and for gene				
CC	therapy. NTAP antagonists are used to treat and prevent a wide range of				
CC	cancers and immune disorders (e.g. AIDS, asthma, Crohn's disease,				

Db	970	TACAGTGGCCCGAGGAGAAAGTGGTCACCTGTCGAGTACCCACCATGAAGAAGATCATATA	1025
Qy	1057	CCATATTTGGGAATTTGCCACAGACAGTATGACATTTGGGTTTGGGGTTTATTTTGAATG	1116
Db	1030	TCCTTTTGGGAATTTGCCACAGACAAATATGACATTTGGGTTTGGGGTGTATTTTGAATG	1089
Qy	1117	GACAGACTCTCCAAATGTCGTCAGTGTGCATGTCTAGTCAGTCCAGTGACGAGGAGGA	1176
Db	1090	GACAGACTCTCCAAACACTGCTGTCCAGGTGCATGTCTAGTCAGTCCAGCATGACGACGA	1149
Qy	1177	GGAGGAGGAGAAATGTCACCTTGTGAAGAAAGCAAAAGCAACGCCACACAGCCTCT	1236
Db	1150	GGAGGAGGAGAAACATCGGTGTGAAGAAAGCAAAAGCAACGCCACACAGCCTTT	1209
Qy	1237	GCTGGATGAGATGTACCTGTGTACCGCGGGGACTGTCTACGAGCAAGTATATGACGSCAG	1296
Db	1210	GCTGGATGAGATGTGCTGTGTACCGAGCGGACTGTCTACGAGGAGTGTATGCTGGCAG	1269
Qy	1297	CCACAGTATCCAGGAGGGAGTCTATCTCCTCAAGTTTGATTAATTCCTACTCTCTGTG	1356
Db	1270	CCATCAATATCCAGGAGAGGAGTCTATCTCCTCAAGTTTGACAACTCTACTCTTTGTG	1329
Qy	1357	GAGGTCCAAGTCGGTCTACTACAGAGTCTATATACTAGATAGACTGCTGTTCCAAAGT	1416
Db	1330	GCGGTCAAAATCAGTCTACTACAGAGTCTATATACTAGATAAAATGTTTACAAAGT	1389
Qy	1417	CCGAGTCCAGGGTTGAGCAACAATGACGTTTAATTT	1454
Db	1390	CTGGAGTCTAGGGTTGGCGAGAAGATGACATTTAATTT	1427
RESULT 4			
AAK53035			
ID	AAK53035 standard; cDNA; 2350 BP.		
XX	AAK53035;		
XX	06-NOV-2001 (first entry)		
DT	Human polynucleotide SEQ ID NO 2564.		
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
OS	Homo sapiens.		
XX	WO200157190-A2.		
PN	09-AUG-2001.		
PD	05-FEB-2001; 2001WO-US04098.		
PF	03-FEB-2000; 2000US-0496914.		
XX	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,		
PI	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WEI; 2001-476283/51.		
DR	P-PSDB; AAM79902.		
DR	Nucleic acids encoding polypeptides with cytokine-like activities.		
PT			

Db 422 TTTTGGGAATTTGCCACAGACAAATTATGACATTTGGTTGGGTGATTTTCAATGGACA 481
QY 1121 GACTCTCCAAATGCTGCTGTCTAGTGTGATGTCAGTCCAGTCCAGGAGGAGGAG 1180
Db 482 GACTCTCCAAACACTGCTGTCTAGCGCTGCTAGTGTGATGTCAGTCCAGCGATCAGCAGGAG 541
QY 1181 GAGGAAGAAATGTCACATTGTGAAGAAAAAGCAAAAAAGAACGCCCAACAGCCTTGCTG 1240
Db 542 GAAGAAGAAACATCGGTGTGTGAAGAGAAAGCCAAAAAGATGCCAACAAGCCTTTGCTG 601
QY 1241 GATGAGATTGTACCTGTGTACCGCGGGGACTGTCTACGAGGAAGTATATGCGAGCGGCCAC 1300
Db 602 GATGAGATTGTGCTGTGTACCGCGGGGACTGTCTATGAGGAGGTATGCTGGCAGCCAT 661
QY 1301 CAGTATCCAGGAGGGGAGTCTATCTCTCAAGTTTGATAATTCCTACTCTCTGTGGAGG 1360
Db 662 CAATATCCAGGAGGAGGAGTCTATCTCTCAAGTTTGATAATTCCTACTCTCTGTGGCGG 721
QY 1361 TCCAGTCCGCTACTACAGAGTCTATTATCTACTAGATAGAGTGTCTTCCAGGTCGGG 1420
Db 722 TCANAATCAGTCTACTACAGAGTCTATTATCTACTAGATAAAAAATGTTGTACAAAGTCTGG 781
QY 1421 AGTCCAGGTTTGAGCACACATGACGTTTAATT 1454
Db 782 AGTCTAGGTTGGGAGAGATGACATTTAATT 815

RESULT 6
AAC77363
ID AAC77363 standard; cDNA; 420 BP.
XX AC AAC77363;
XX
XX
XX 08-FEB-2001 (first entry)
XX Human ORFX ORF2918 polynucleotide sequence SEQ ID NO:5835.
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antiprosclatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antitumor; antibacterial; antifungal; antineumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX Homo sapiens.
XX OS
XX WO200058473-A2.
XX PD
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US08621.
XX
XX 31-MAR-1999; 99US-0127607.
XX PR 02-APR-1999; 99US-0127636.
XX PR 05-APR-1999; 99US-0127728.
XX PR 30-MAR-2000; 2000US-0540763.
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XX (CURA-) CURAGEN CORP.
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XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
XX DR P-PSDB; ABA43154.
XX
XX Novel nucleic acids and peptides derived from open reading frame X.
PT

PT useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
XX Claim 5; Page 5005; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in ABA40237 to ABA43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiprosclatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;
CC antithyroid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 420 BP; 134 A; 69 C; 127 G; 88 T; 2 other;

Query Match 20.1%; Score 293.2; DB 21; Length 420;
Best Local Similarity 89.3%; Pred. No. 9.2e-69;
Matches 316; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 97 AGTAAAGATGCAAGGCTTTTCATCCAACTTATGAAGAAAAAAGTCTGTCGCACT 156
Db 66 AGAAAAAGATGCAAGGATTTTCATCCAACTTATGAAGAAAAATTTGAGCTTTGGCACT 125

QY 157 GCATGAAGCAAGTCTTTTGGGCCCATATAACCCAGACACGTCCTCCCTGAGTTGGATTCTT 216
Db 126 GCATGAAGCAAGTCTTTTGGGCCCATATAATCCAGACACTTCTCTGAGTTGGATTCTT 185

QY 217 TCATGTTTGGGAATGATAGGAGGAGAGATGGCGAGCTCTGGGAACATGTCACAGA 276
Db 186 TCATGTTTGGGAATGATAGGAGGAGAGATGGCGAGCTCTGGGAACATGTCACAGA 245

QY 277 GGATCCCATGTTAGAGTTTGTGAAGCTTCTAAATAGTGTCTCTCTCTCGGCATA 336
Db 246 GGATCCCATGTTAGAGTTTGTGAAGCTTCTAAATAGTGTCTCTCTCTCGGCATA 305

QY 337 TGTTCCTGCTCCACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
Db 306 TGTTCCTGCTCCACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365

QY 397 GCGAAGCGGCGTGAAG 450
Db 366 GCGAAGCGGCGTGAAG 419

RESULT 7
AAK53762/c
ID AAK53762 standard; cDNA; 278 BP.
XX AC AAK53762;
XX
XX 16-NOV-2001 (first entry)
XX
XX Murine transport and binding associated protein encoding cDNA SEQ ID 327.
DE
XX Murine; liver; gene library; amino acid synthesis; binding protein;
KW cell metabolism; energy metabolism; fatty acid metabolism; synthesis;
KW phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide;
KW replication; transcription; translation; transport protein; ss.
XX

QY 894 GACCAAAAG 902
|||||
Db 433 GACCAAAAG 441

RESULT 11
ID AAK77371/c
AAK77371 standard; DNA; 4384 BP.

XX
AC AAK77371;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32183.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 18-MAR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 14-AUG-2000; 2000US-0224518.
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PR 30-AUG-2000; 2000US-0228924.
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PR 01-SEP-2000; 2000US-0229345.
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PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 02-OCT-2000; 2000US-0236802.
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PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
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PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 32183; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human Immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 4384 BP; 1434 A; 933 C; 758 G; 1259 T; 0 other;

Query Match 8.8%; Score 129; DB 22; Length 4384;
Best Local Similarity 90.2%; Pred. No. 4.5e-24;
Matches 138; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 97 ACTAAAGATGCAAGCCTTTCATCCACCTATGCAAGAAACTGAAGTTCGTGGCACT 156
DB 4384 AGAAAAAGATGCAAGCATTTCATCCACCTATGCAAGAAACTGAAGTTCGTGGCACT 4325

QY 157 GCATTAAGCAAGTCTTTTGGGCCCATATAACCCACACACGTCCTCGAGTTGGATTCTT 216
DB 4324 GCATTAAGCAAGTCTTTTGGGCCCATATAATCCACACACTTGTCTCGAGTTGGATTCTT 4265

QY 217 TGATCTGTTGGGGAATGATAGGAGGAGAGATG 249
DB 4264 TGATCTGTTGGGGAATGACAGGAGTACAGTG 4232

RESULT 12
ID AAK24345
XX ABK24345 standard; cDNA; 527 BP.
XX
XX AC ABK24345;
XX

DT 09-APR-2002 (first entry)
XX
DE DNA encoding human lung cancer protein, Seq ID No 32.
KW Human; lung cancer; cytostatic; vaccine; gene; ss.
XX
OS Homo sapiens.
XX WO200192525-A2.
PN 06-DEC-2001.
PD 25-MAY-2001; 2001WO-US17066.
XX 26-MAY-2000; 2000US-207485P.
PF 06-SEP-2000; 2000US-230475P.
PR (CORI-) CORIXA CORP.
XX
XX Harlocker SL, Wang T, Bangur CS, Klee JI, Switzer A;
PI WPI; 2002-122068/16.
DR
XX New lung tumour polypeptides and polynucleotides, useful in
PT pharmaceutical compositions, such as vaccines, for treating or
PT preventing lung cancer, or as probes or primers for nucleic acid
PT hybridisation
XX
XX Claim 1; Page 138; 179pp; English.
PS
XX The invention relates to novel human lung cancer polynucleotide (I)
CC and polypeptides (II). (I) and (II) are useful in pharmaceutical
CC compositions, such as vaccines, for the diagnosis and treatment of lung
CC cancer. The polynucleotides are also useful as probes or primers for
CC nucleic acid hybridisation. ABK24314-ABK24397 represent human lung
CC cancer coding sequences of the invention.
XX
SQ Sequence 527 BP; 141 A; 103 C; 112 G; 160 T; 11 other;

Query Match 7.8%; Score 113.4; DB 24; Length 527;
Best Local Similarity 84.08%; Pred. No. 2.6e-20;
Matches 126; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1305 ATCCAGGAGGGAGTCTATCTCTCAAGTTTGATAATTCCTACTCTCTGTGGAGTCCA 1364
DB 1 ATCCAGGAGGAGGAGTCTATCTCTCAAGTTTGACAACCTCTACTCTTTGTGGCGGCAA 60

QY 1365 AGTCGCTCTACTACAGAGTCTATTACTATAGATAGAGTCTGTTCGAAGTCCGGAGTC 1424
DB 61 AATCAGTCTACTACAGAGTCTATTACTATAGATAAAATGTNGGTACAAAGTCTGGAGTC 120

QY 1425 CAGGTTTGACGACACATGACGTTTAATTT 1454
DB 121 TAGGTTGGGCAGAGATGACATTTAATTT 150

RESULT 13
ID ABA62955/c
XX ABA62955 standard; DNA; 554 BP.
XX
XX AC ABA62955;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #11260.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX OS Homo sapiens.
XX
XX WO200157277-A2.
XX
XX PD 09-AUG-2001.

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SUMMARIES

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C 1	99.6	6.8	7218	1 US-08-232-463-14	Sequence 14, Appl
2	74.2	5.1	3489	2 US-08-728-323A-1	Sequence 1, Appl
3	74.2	5.1	3489	4 US-09-298-588-1	Sequence 1, Appl
C 4	74.2	5.1	32207	2 US-08-770-379-20	Sequence 20, Appl
C 5	74.2	5.1	32207	4 US-08-757-669A-20	Sequence 20, Appl
C 6	74.2	5.1	32207	4 US-09-230-371A-20	Sequence 20, Appl
7	72.6	5.0	1926	4 US-09-249-585A-2	Sequence 2, Appl
8	72.6	5.0	2580	3 US-09-050-883-2	Sequence 2, Appl
9	72.6	5.0	2580	4 US-09-359-081-2	Sequence 2, Appl
C 10	72.6	5.0	5452	2 US-09-130-114-1	Sequence 1, Appl
11	72.6	5.0	9600	4 US-08-910-647-1	Sequence 1, Appl
12	72.6	5.0	9600	4 US-08-620-925-1	Sequence 1, Appl
13	72.6	5.0	10596	1 US-07-884-811-15	Sequence 15, Appl
14	72.6	5.0	10596	1 US-07-885-971-15	Sequence 15, Appl
15	72.6	5.0	10596	1 US-08-087-783A-15	Sequence 15, Appl
16	72.6	5.0	10596	1 US-08-194-088B-15	Sequence 15, Appl
17	72.6	5.0	10596	2 US-08-194-087-15	Sequence 15, Appl
18	72.6	5.0	10596	5 PCT-US93-04648-15	Sequence 15, Appl
19	70.8	4.9	543	6 5273901-5	Patent No. 5273901
20	69.4	4.8	533	6 5482709-5	Patent No. 5482709
C 21	69.4	4.8	16442	3 US-08-781-891-208	Sequence 208, App
C 22	65.6	4.5	51259	3 US-08-781-891-209	Sequence 208, App
23	63.6	4.4	9551	1 US-08-056-200-93	Sequence 93, Appl
24	63.6	4.4	9551	2 US-08-800-644-93	Sequence 93, Appl
25	60.6	4.2	289	4 US-09-007-005-17	Sequence 17, Appl
26	60.6	4.2	289	4 US-09-244-796-17	Sequence 17, Appl
27	56.8	3.9	397	3 US-09-253-691-3	Sequence 3, Appl

28	56	3.8	4266	4 US-09-651-011A-3	Sequence 3, Appl
29	54.8	3.8	939	1 US-08-285-440-10	Sequence 10, Appl
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31	54.8	3.8	1599	1 US-08-285-440-11	Sequence 11, Appl
32	54.8	3.8	1599	1 US-08-630-349-11	Sequence 11, Appl
33	54.8	3.8	1677	1 US-08-285-440-12	Sequence 12, Appl
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37	54.8	3.8	2215	1 US-08-285-440-14	Sequence 14, Appl
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40	54.4	3.7	248	4 US-09-244-796-32	Sequence 32, Appl
41	54.4	3.7	277	4 US-09-007-005-3	Sequence 3, Appl
42	54.4	3.7	277	4 US-09-244-796-3	Sequence 3, Appl
43	54.4	3.7	2301	1 US-08-306-691B-23	Sequence 23, Appl
44	54.4	3.7	2301	5 PCT-US93-06251-78	Sequence 78, Appl
45	53.8	3.7	152331	3 US-09-128-155-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT29pt-F1s
US-08-232-463-14

Query Match 6.8%; Score 99.6; DB 1; Length 7218;


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; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 32207 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20

Query Match          5.1%; Score 74.2; DB 4; Length 32207;
Best Local Similarity 50.3%; Pred. No. 1.9e-10;
Matches 236; Conservative 0; Mismatches 228; Indels 5; Gaps 2;

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DB 20120 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGC 20061
QY 417 AAGAACGAGAGCGCTGCRAAAGGAAGAAAGAACGGGAAGCCAGAGGAGGAGACCGGC 476
DB 20060 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 20001
QY 477 TGAGACGGGAGGAGGAGAGAGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC 536
DB 20000 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19941
QY 537 AAAAGCAGCAGATAATTGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCACGACGATATG 596
DB 19940 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19881
QY 597 CAGCCCAGCAGTAT---CCAGGGAACCTACGAACAACAGCAGATTCCTCCGCCAGCTGC 653
DB 19880 AGGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGC 19821
QY 654 AGGAGCAGCACTATCAGCAGTATAAACACCAG--GCAGAGCAAACCCACCTGCACAACA 711
DB 19820 AGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATG 19761
QY 712 ACAGGCAGCATTCACAGAAACAGCAAGTAGTGATGGCTGGGGCATCATTTGCTTCATC 771
DB 19760 AGCAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGGAGGAGGAGCAGG 19701
QY 772 ATCAAAGGTGAACACAGCTCGCAAGTAGTATACACTGTCTCAGTTTAATGGA 820
DB 19700 AGCAGGAGTTAGAGGAGCAGCAGGAGTTAGAGGATCAGGAGCAGGA 19652

RESULT 6
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; Sequence 20, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; PRIOR FILING DATE: 1999-11-17
; PCT FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver.. 2.0
; SEQ ID NO 20
; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match          5.1%; Score 74.2; DB 4; Length 32207;
Best Local Similarity 50.3%; Pred. No. 1.9e-10;
Matches 236; Conservative 0; Mismatches 228; Indels 5; Gaps 2;

QY 357 AGAAGGAAGAAGAAAGAAAGAACGCGGAGGAGGACGCAAGCGCTGAAGAGG 416
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QY 477 TGAGACGGGAGGAGGAGAGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC 536
DB 20000 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19941
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DB 19940 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19881
QY 597 CAGCCCAGCAGTAT---CCAGGGAACCTACGAACAACAGCAGATTCCTCCGCCAGCTGC 653
DB 19880 AGGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGC 19821
QY 654 AGGAGCAGCACTATCAGCAGTATAAACACCAG--GCAGAGCAAACCCACCTGCACAACA 711
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QY 712 ACAGGCAGCATTCACAGAAACAGCAAGTAGTGATGGCTGGGGCATCATTTGCTTCATC 771
DB 19760 AGCAGCAGCAGGATGAGCAGCAGCAGCAGCAGCAGCAGGAGGAGGAGCAGG 19701
QY 772 ATCAAAGGTGAACACAGCTGGGAGCAAGTAGTATACACTGTCTCAGTTTAATGGA 820
DB 19700 AGCAGGAGTTAGAGGAGCAGCAGGAGTTAGAGGATCAGGAGCAGGA 19652

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US-09-230-371A-20/c
; Sequence 20, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; PRIOR FILING DATE: 1999-11-17
; PCT FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver.. 2.0
; SEQ ID NO 20
; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match          5.1%; Score 74.2; DB 4; Length 32207;
Best Local Similarity 50.3%; Pred. No. 1.9e-10;
Matches 236; Conservative 0; Mismatches 228; Indels 5; Gaps 2;

QY 357 AGAAGGAAGAAGAAAGAAAGAACGCGGAGGAGGACGCAAGCGCTGAAGAGG 416
DB 20120 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGC 20061
QY 417 AAGAACGAGAGCGCTGCRAAAGGAAGAAAGAACGGGAAGCCAGAGGAGGAGACCGGC 476
DB 20060 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 20001
QY 477 TGAGACGGGAGGAGGAGAGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC 536
DB 20000 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19941
QY 537 AAAAGCAGCAGATAATTGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCACGACGATATG 596
DB 19940 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19881
QY 597 CAGCCCAGCAGTAT---CCAGGGAACCTACGAACAACAGCAGATTCCTCCGCCAGCTGC 653
DB 19880 AGGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGC 19821
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DB 19700 AGCAGGAGTTAGAGGAGCAGCAGGAGTTAGAGGATCAGGAGCAGGA 19652

RESULT 6
US-09-230-371A-20/c
; Sequence 20, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; PRIOR FILING DATE: 1999-11-17
; PCT FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver.. 2.0
; SEQ ID NO 20
; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20

Query Match          5.1%; Score 74.2; DB 4; Length 32207;
Best Local Similarity 50.3%; Pred. No. 1.9e-10;
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QY 357 AGAAGGAAGAAGAAAGAAAGAACGCGGAGGAGGACGCAAGCGCTGAAGAGG 416
DB 20120 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGC 20061
QY 417 AAGAACGAGAGCGCTGCRAAAGGAAGAAAGAACGGGAAGCCAGAGGAGGAGACCGGC 476
DB 20060 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 20001
QY 477 TGAGACGGGAGGAGGAGAGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC 536
DB 20000 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19941
QY 537 AAAAGCAGCAGATAATTGGCAGCTTTAAACTCGCAGACTGCCGTGCAATTCACGACGATATG 596
DB 19940 AGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGC 19881
QY 597 CAGCCCAGCAGTAT---CCAGGGAACCTACGAACAACAGCAGATTCCTCCGCCAGCTGC 653
DB 19880 AGGAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGC 19821
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QY 712 ACAGGCAGCATTCACAGAAACAG
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QY 476 CTGAGACGGGAGGAGAGAGCGGCGGATAGAGAGAGAGAGGCTTCGGCTGGAACAG 535
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Db 2652 CAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGAGGGGCAGGAGGGGGG 2711

QY 596 GCAGCCCAGCAGTATCCAGGGNACTACGAACACAGCAGATTCTCATCGCCAGCTGCAG 655
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Qy 716 GCAGCATTACAAACAGCAAGAAGTAGTG 745
Db 427 GAAGAGGAAGAAGAGGAGGAAGAAGAGAG 456

RESULT 14
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; Sequence 73, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-101-487-73

Query Match 4.2%; Score 62; DB 9; Length 530;
Best Local Similarity 47.4%; Pred. No. 2.8e-07;
Matches 185; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

Qy 356 GAGAAGGAAGAAGAAGAAAAGAGCGGAGGAGGAGCGAGGAGCGAGCGTGAAGAG 415
Db 464 GAAGAGGAAGAGAGGAGGAAGAAGAAGAGGAGGAAGAGAGAGGAGGAAGAAGAG 405
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Db 404 GAAGAGGAAGAAGAGGAGGAAGAAGAAGAGGAGGAAGAAGAGGAGGAAGAAGAG 345
Qy 476 CTGAGACGGGAGGAGAGAGAGCGCGGATAGAGGAAGAGAGGCTTCGCGTGAACAG 535
Db 344 GAAGAGGAAGAAGAGGAGGAAGAAGAAGAGGAGGAAGAGAGGAGGAAGAAGAG 285
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; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 60/277,705
; PRIOR FILING DATE: 2001-03-21
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; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
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; LOCATION: (1)..(528)
US-10-101-487-69

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Matches 191; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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EST.
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NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10372 row: k column: 08
High quality sequence stop: 680.
Location/Qualifiers
1. 757

FEATURES
source

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Note: this is a NIH_MGC Library."
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5', mRNA sequence.
ACCESSION BQ223172
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ORGANISM Homo sapiens
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AUTHORS Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
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http://image.llnl.gov
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High quality sequence stop: 20
High quality sequence stop: 395.
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 297 a 197 c 264 g 174 t
ORIGIN
Query Match 38.1%; Score 555.6; DB 14; Length 932;
Best Local Similarity 82.8%; Pred. No. 4.7e-121;
Matches 671; Conservative 0; Mismatches 134; Indels 5; Gaps 3;
Qy 97 AGTAAAGATGGAAAGCTTTTCATCCAACTATGAAGAAAACATGCGTGGCACT 156
Db 116 AGAAAAGATGGAAAGCTTTTCATCCAACTATGAAGAAAACATGCGTGGCACT 175
Qy 157 GCATAAGCAAGTCTTTTGGGCCATATAACCCAGACAGTCCCTGAGGTGGATTCTT 216
Db 176 GCATAAGCAAGTCTTTTGGGCCATATAATCCAGACACTTGTCTGAGGTGGATTCTT 235
Qy 217 TGATGTGTGGGAATGATAGGAGAGAGATGGGAGCTCTGGGAAACATGTCCAAGGA 276
Db 236 TGATGTGTGGGAATGATAGGAGAGAGATGGGAGCTCTGGGAAACATGTCTAAGA 295
Qy 277 GGATGCCATGTAGAGTTTGTGAAGCTTCTAAATAGTGTGTCTCTCTCTCGGCATA 336
Db 296 GGATGCCATGTAGAGTTTGTGAAGCTTCTAAATAGTGTGTGTCTCTCTCTCAACATA 355
Qy 337 TGTTCGCTCCACAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
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Qy 457 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
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Qy 517 GAGGCTTCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
Db 536 AAGGCTTCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
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QY	1259	TACCGGGGGACTGTCCACGAGGAAGTATATGACGAGCCACACAGTATCCAGGGAGGGGA	1318
Db	421	TACCCAGGGGACTGTCTAGGAGAGGTGTATGCTGGCAGCCATCAATATCCAGGGAGAGGA	480
QY	1319	GTCTATCTCTCAAGTTTGATAAATTCCTACTCTCTGTGGAGTCCCAAGTCCCTCTACTAC	1378
Db	481	GTCTATCTCTCAAGTTTGACAACTCTACTCTTTGTGGCGGTCAAAATCACTCTACTAC	540
QY	1379	AGAGTCTATTATAGATAGAGCTGTGTTCCCAAGGTCGCGAGTCCAGGGTTGAGCACA	1438
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QY	1439	ACATGACGTTTAATTT 1454	
Db	601	AGATGACATTTAATTT 616	
RESULT 6			
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DEFINITION	602669271f1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792145 5',		
ACCESSION	BG705952		mrna sequence.
VERSION	BG705952.1		GI:13980813
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 707)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-re@mail.nih.gov		
	Tissue procurement: Miklos Palkovits, M.D., Ph.D.		
	cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki		
	Toshiyuki and Piero Carninci (RIKEN)		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM10669 row: n column: 18		
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	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pBluescriptR (modified		
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) ; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',		
	size-selected for average insert size 2.3 kb and		
	normalized to ROT 5. This is a primary library enriched		
	for full-length clones and constructed using the		
	Cap-trapper method (Carninci, in preparation). Library		
	constructed by M. Brownstein (NIH/NHGRI, National		
	Institutes of Health). Note: this is a NIH_MGC Library."		
BASE COUNT	217 a 143 c 178 g 169 t		
ORIGIN			
Query Match	33.4%;	Score 487.6;	DB 12; Length 707;
Best Local Similarity	87.3%;	Pred. No. 6e-105;	
Matches 557;	Conservative 0;	Mismatches 79;	Indels 2; Gaps 2;

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Db	4	GAACAGGCCAAACACACACTGACAGCTCCGAAAAAGAACTGGAACCAAGAGCTCGAGAA	63
QY	878	GAAGCTTTGGAAATGGACCAAAAGACTCTCTCCAGTGATTGACAGCTCCATCCCATGTTGG	937
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QY	938	ACAAGACACCAAAATCAAAAGACTTTTAAAGAGAAGATTCCGCCAGGATGCAGATTCTCTGATT	997
Db	124	ACACGACCTCAGATCAAAAGACTTCAACAGAGAAGATTACGAGGATGCAGATTCCCTGATT	183
QY	998	ACAGTACGTCGAGGAGAAGTCGTACCGTCGAGTCCCGACTFCATGAGGAGAAGATCATAC	1057
Db	184	ACAGTGGGCCGAGGAGAAGTGGTCACTCTCGAGTACCCACCACCATGAAGAAGGATCATAT	243
QY	1058	CTATTTTGGGAATTTGCCACAGACAGATTATGACATTTGGGTTTGGGGTTTATTTTGAATGG	1117
Db	244	CTCTTTTGGGAATTTGCCACAGACAAATTTATGACATTTGGGTTGCGGGTGTATTTTGAATGG	303
QY	1118	ACAGACTCTCCAATGCTGCTCAGTGTGCATGTCACTGAGTCCAGTGACGAGGAGGAG	1177
Db	304	ACAGACTCTCCAACACACTGCTGTACGCGTGCATGTCACTGAGTCCAGCGATGACACGAG	363
QY	1178	GAGGAGGAAGAAATGTCACTTGTGAAGAAAAGCAAAAAGAACGCCAACAAAGCTCTG	1237
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QY	1238	CTGGATGAGATGTACCTGTGTACCGCGGGGACTGTACGAGGGAAGTATATCCAGGCAGC	1297
Db	423	CTGGATGAGATGTGCTGCTGTACCGACGGGACTGTCTATGAGGAGGTGTATGCTGGCAGC	482
QY	1298	CACAGTATCCAGGAGGGGAGTCTATCTCTCAAGTTTGATAATTCCTACTCTCTGTGG	1357
Db	483	CATCAATATCCAGGAGGAGGAGTCTATCTCTCAAGTTTGACAACCTCTACTCTTTGG	542
QY	1358	AGGTCCAAAGTCGCTACTACAGCTCTATATATAGAT-AGAGCTGCTTCCAAGT 1416	
Db	543	CGGTCAAAATCAGTCTACTACAGAGTCTATTATAGATAACAATAATGCTGTACAAAGT	602
QY	1417	CCGGAGTCCAGGTTGAGCACAAACATGACGTTTAATTT 1454	
Db	603	CTGGAGTCTAGGTTGGGCAGAGAAGATGACATTTAATTT 640	
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LOCUS	BB704602	493 bp	mrna linear EST 11-OCT-2001
DEFINITION	BB704602 RIKEN full-length enriched, in vitro fertilized eggs Mus		
ACCESSION	musculus cDNA clone 7420465P14 3', mRNA sequence.		
VERSION	BB704602		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 493)		
AUTHORS	Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanezaki,T.,		
	Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii		
	,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,		
	Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.		
	,Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,		
	Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa		
	,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.		
	, Watanishi,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.		
	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.		
	2001)		
TITLE	Unpublished (2001)		
JOURNAL	Contact: Yoshihide Hayashizaki		
COMMENT	Laboratory for Genome Exploration Research Group, RIKEN Genomic		
	Sciences Center(GSC), Yokohama Institute		
	The Institute of Physical and Chemical Research (RIKEN)		

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/tissue_type="tumor, biopsy sample"
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/lab_host="DH10B"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 220 a 139 c 197 g 93 t
ORIGIN

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Best Local Similarity 92.5%; Pred. No. 6e-95; Indels 18; Gaps 12;
Matches 602; Conservative 0; Mismatches 31;
QY 314 TGTGTCTCTCTCTCGGCATATGTTGCTCCACAGATAGAGAAGGAAGAAAGAG 373
Db 1 TGTGTCTCTCTCTCTCGGCATATG-TGCGTCCACAGATAGAGAAGGAAGAAAGAG 59
QY 374 AAA-AGAAGAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 432
Db 60 AAGAGAGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119
QY 433 GCAAGAGAGAGAGAGAGAGCGGAGCG-AGAGGAGAGAGCGGCTGACGCGGAGGAGG 491
Db 120 GCAAGAGAGAGAGAGAGCGGAGCGGAGGAGGAGAGCGGCTGACGCGGAGGAGG 179
QY 492 AAGAGAGGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACGCAAAAGCAGCAGATAA 551
Db 180 AAGAGAGGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACGCAAAAGCAGCAGATAA 239
QY 552 TGGCAGCTTTAAATCGGCAGA--CTGCCGTGCAATTCAGC-AGTATGAGCCCAAGC-AG 607
Db 240 TGGCAGCTTTAAACTCGCAAGAGCGTGCCTGCAATTCCAGCGAGTATGACGCCCAAG 299
QY 608 TATCCAGGGAAGTACGACCAACAGC-AGATCTCATCGCCAGCTGC-AGGAGCAG-CA 663
Db 300 TATCCAGGGAAGTACGACCAACAGCAGCGAGATTTCTCATCGCCAGCTGCGAGGAGCAGTCA 359
QY 664 CTATCAGCAGTATAACACAGGAGGAGCAAAACCCAACTTCACACAA-- ---CAGGCGAG 719
Db 360 CTATCAGCAGTATATGACGCGAGTTGATATCAAGTCCAGCTTTCGCAACAACAGCAGGCGAG 419
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Db 420 CATTACAGAAACAGCAAGAGTAGTATGATGGCTGGGGCATCATTTGCCATCATCAAGG 479
QY 780 TGAACACAGCTGGACCAAGTATACACTGT--CAGTTAATGACAGGCGCAAAACCCACAC 837
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RESULT 11
BF797451
LOCUS BF797451 984 bp mRNA linear EST 12-JAN-2001
DEFINITION 602527111F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4340355 5',
mRNA sequence.
ACCESSION BF797451
VERSION BF797451.1 GI:12102505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 984)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: Louis Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9952 row: f column: 04
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Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 283 a 192 c 235 g 274 t
ORIGIN

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QY 1266 GGGACTGTCCAGGAAGTATATGACGAGCAGCCAGTATCCAGGGAGGGGAGGAGTCTATTC 1325
Db 361 GGGACTGTCCAGGAGGTTGATGCTGGCAGCCATCAATATCCA-GGAGAGGAGTCTATC 419
QY 1326 TCCTCAAGTTTGATTAATTCCTACTCTCTGTGAGGTCCAAAGTCCCGTCTACTACAGAGTCT 1385
Db 420 TCCTCAAGTTTGACAACTCTACTCTTTGTGGCGGTCAAAATCAGTCTACTACAGAGTCT 479
QY 1386 ATTATACATAGTAGAGCTGCTGTTCCAAAGGTCGCGGAGTCCAGGTTGAGCAACAATGAC 1445
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RESULT 12
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DEFINITION PMI-BT0759-200700-006-c03 BT0759 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE694778
VERSION BE694778.1 GI:10081938
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-PM1-BT0759-200
700-006-c03&t3=2000-07-20&t4=1)
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High quality sequence stop: 519.
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into the pUC 18 vector. Reverse transcription of tissue
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stringency conditions."
BASE COUNT 160 a 110 c 138 g 111 t
ORIGIN
source
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Best Local Similarity 88.0%; Pred. No. 2.2e-85;
Matches 441; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 905 TCTCTTCAGTGATTCAGCTCCATCCATGTGGACAGACCAACCAATCAAGACTTTAA 964
Db 79 TCTCTCCAGTAATAGCAGCTCCATCCATGTGGACAGACCTCGATCAAGACTTCAA 138
QY 965 GAGAAATTCGGCAGGATCGCATCTGTGATTACAGTACGTGAGGAGAAATCGTCACC 1024
Db 139 GAGAAGATTCAGCAGGATCGATTCGCTGATTACAGTGGCGCGAGGAGAGTGCTACT 198
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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(without alignments)
10870.710 Million cell updates/sec

Title: US-09-762-594-2

Perfect score: 1459

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

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38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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3	1079.6	74.0	3598	9	AB043587	AB043587 Homo sapi
4	890.4	61.0	3049	9	BC034563	BC034563 Homo sapi
5	287.2	19.7	18140	10	AF501319	AF501319 Mus muscu
6	246.2	16.9	63971	2	AC121292	AC121292 Mus muscu
c 7	238	16.3	140409	2	AC044825	AC044825 Homo sapi
c 8	238	16.3	181719	2	AL592045	AL592045 Homo sapi
c 9	238	16.3	232180	2	AC021883	AC021883 Homo sapi
c 10	228.4	15.7	174143	2	AC126290	AC126290 Rattus no
c 11	211.4	14.5	2235	9	AK057118	AK057118 Homo sapi
c 12	204.4	14.0	934	6	AX339070	AX339070 Sequence
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c 14	150.8	10.3	3547	9	AK095650	AK095650 Homo sapi
c 15	150	10.3	882	6	AX400067	AX400067 Sequence
c 16	113.4	7.8	527	6	AX339069	AX339069 Sequence
c 17	110.6	7.6	210204	9	AC007954	AC007954 Homo sapi
c 18	102.2	7.0	227588	2	AC094571	AC094571 Rattus no
c 19	100.8	6.9	1779	3	AY051848	AY051848 Drosophi
c 20	99.8	6.8	150641	3	CEY41E3	295559 Caenorhabdi
c 21	99.6	6.8	7218	6	I66494	I66494 Sequence 14
c 22	95.6	6.6	155662	2	AC112388	AC112388 Rattus no
c 23	95.6	6.6	189461	2	AC119627	AC119627 Rattus no
c 24	95.6	6.6	191841	2	AC121374	AC121374 Rattus no
c 25	95.2	6.5	84472	2	AC096684	AC096684 Takifugu
c 26	95	6.5	264522	2	AC090437	AC090437 Mus muscu
c 27	94	6.4	204259	2	AC110817	AC110817 Mus muscu
c 28	93.8	6.4	184865	2	AL807824	AL807824 Mus muscu
c 29	93.6	6.4	177035	2	AC099443	AC099443 Rattus no
c 30	93.4	6.4	190594	10	AL606965	AL606965 Mouse DNA
c 31	93.2	6.4	170985	2	AC096032	AC096032 Rattus no
c 32	92.6	6.3	225045	2	AL833803	AL833803 Mus muscu
c 33	92.4	6.3	176030	2	AC129650	AC129650 Rattus no
c 34	92.4	6.3	287058	2	AC095595	AC095595 Rattus no
c 35	92.2	6.3	195673	2	AL807807	AL807807 Mus muscu
c 36	91.8	6.3	180418	2	AC106674	AC106674 Rattus no
c 37	91.8	6.3	272545	2	AC090533	AC090533 Mus muscu
c 38	91.4	6.3	131346	2	AC119558	AC119558 Rattus no
c 39	91.4	6.3	197247	2	AC125713	AC125713 Rattus no
c 40	91	6.2	261604	2	AC119819	AC119819 Mus muscu
c 41	90.2	6.2	168210	2	AC116700	AC116700 Mus muscu
c 42	90	6.2	82400	10	AC090495	AC090495 Genomic s
c 43	89.8	6.2	186559	10	AL606742	AL606742 Mouse DNA
c 44	89.6	6.1	107637	2	AC094679	AC094679 Rattus no
c 45	89.2	6.1	130580	2	AC119765	AC119765 Rattus no

ALIGNMENTS

RESULT: 1
AF022770
LOCUS AF022770 1543 bp mRNA linear ROD 11-APR-2002
DEFINITION Mus musculus peripheral benzodiazepine receptor associated protein
(Pap7) mRNA, complete cds.
ACCESSION AF022770
VERSION AF022770.2 GI:7545290
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1543)
AUTHORS Li, H., Degenhardt, B., Tobin, D., Yao, Z. X., Tasken, K. and Papadopoulos, V.


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QY 1237 GCTGGATGAGATTGTACCTGTGTACCGGGGAGCTGTACAGGAGAGTATATGTCAGGCAG 1296
Db 1480 GCTGGATGAGATTGTGCTGTGTACCGAGCGGACTGTATGAGGAGTGTATCTCTGGCAG 1539
QY 1297 CCACGAGTATCAGGAGGAGTCTATCTCTCAAGTTTGATTAATCTCTACTCTCTGTG 1356
Db 1540 CCATCAATATCAGGAGGAGTCTATCTCTCAAGTTTGATTAATCTCTACTCTCTGTG 1599
QY 1357 GAGGTCCAAGTCCGCTACTACAGAGTCTATTATATCTAGATAGAGTGTCTTCCAAGT 1416
Db 1600 GCGGTCAAAATCAGTCTACTACAGAGTCTATTATCTAGATAAAATGTTGTACAAAGT 1659
QY 1417 CCGGAGTCCAGGTTGAGCACACATGAGCTTTAATTT 1454
Db 1660 CTGGAGTCTAGGTTGGCAGAGATGACATTTAATTT 1697

RESULT 4
BC034563 3049 bp mRNA linear PRI 26-JUL-2002
DEFINITION Homo sapiens, similar to golgi complex associated protein 1, 60
kDa, clone IMAGE:3858463, mRNA, partial cds.
ACCESSION BC034563
VERSION BC034563.1 GI:21961496
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3049)
Strausberg,R.
Direct Submission
Submitted (24-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/BNP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 21 Row: C Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

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/notes="Vector: pCMV-SPORT6"
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60 kDa"
/protein_id="AAH34563.1"
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/translation="RTRGCHLFSTYVASHKTEKEFEQKKRKEEERREERLERLQ
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TAVSVHYSESDDDEBEENIGCEKAKKNANKPLLEIVPVYRRDCHEEVYAGSHQY
PGRVYLLKFDNSLSLWRSKSVYRVYITR*
BASE COUNT 963 a 522 c 633 g 931 t
ORIGIN
Query Match 61.0%; Score 890.4; DB 9; Length 3049;
Best Local Similarity 86.3%; Pred. No. 8.1e-216;
Matches 984; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 315 GTTGTCTCTCTCTCGCATATGTTGGCTCCACAGATAGAGGAAGAGAGAGA 374
Db 11 GGTGCCATCTCTTCAACATATGTTGGTCCCAAAATAGAGAAGAGCAAGAA 70
QY 375 AAAGAAGAAAGCGGAGGAGGAGCGAGCGGTGGAAGAGGAAGAGAGCGGTGC 434
Db 71 AAAAAGGAAGGAGGAGGAGGAGCGGAGCGGTGGAAGAGGAAGAGAACGTCTGC 130
QY 435 AAAAGGAAGAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 494
Db 131 AAAAGGAGAGAGAAACGTAGAGAGAGAGAGGAAAGGCTTCAGCGGAGGAGAG 190
QY 495 AGAGCGCGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGG 554
Db 191 AAAGCAGCGGATACAGAAAGAAAGGCTTCGGTGGAGCAGCAAAAGCAGCAGATAATGG 250
QY 555 CAGCTTTAAATCGCAGACTGCCGTGCAATCCAGCAGTATCCAGCCAGCAGTATCCAG 614
Db 251 CAGCTTTAAATCGCAGACTGCCGTGCAATCCAGCAGTATCCAGCCAGCAGTATCCAG 310
QY 615 GGAATACGAAACAGCAGAGTCTCATCCGCGCAGCTGCAGGAGCAGCAGTATCAGCAGT 674
Db 311 GGAATACGAAACAGCAGAGTCTCATCCGCGCAGTTCAGGAGGAGCAACACTATCAGCAGT 370
QY 675 ATAAACACGAGCAGGAGCAAAACCACTGACACAAACAGCAGCAGTATACAGAAACAGC 734
Db 371 ACATGAGCAGTGTATCAAGTCCAGCTTGACACGACGAGCAGCAGTATACAGAAACAGC 430
QY 735 AAGAAGTAGTGTGCTGGGCGATCATGTCCTGTCATCATCAAGGTGAACAGCAGTGGAG 794
Db 431 AGGAAGTAGTGTGCTGGGCTCTCTCTGCTTACATCATCAAAAGTGAATGCAACTGAC 490
QY 795 CAAGTGATACACTGTCAGTTAATGACAGCGCCAAACCCACACTGAAATTCGGAAGAG 854
Db 491 CAAGTAATATGATGTCAGTTAATGACAGCGCCAAACCCACACTGACAGCTCCGAAAGAG 550
QY 855 TCCTTGAGCCAGAAGCTGCAGAAAGAGCGCTTGGAATAATGGACCAAAAGACTCTCTCCAG 914
Db 551 AACTGGAACCAAGCTGCAGAAAGAGCGCTTGGAATAATGGACCAAAAGACTCTCTCCAG 610
QY 915 TGATTGAGCTCCATCCATGTGGACAAGACACAAATCAAGACTTTAAAGAGAGATTC 974
Db 611 TAATGAGCTCCATCCATGTGGACAGCAGCTCAGATCAAAAGACTTCAAAAGAGAGATTC 670
QY 975 GGCAGGATCAGATCTGTGATTACAGTACGTCGAGGAGAGTCTGTCACCGTCCGAGTCC 1034
Db 671 AGCAGGATCAGATCTCCGTGATTACAGTGGCGGAGGAGAGTGTGTCAGTGTGAGTAC 730
QY 1035 CGACTCATGAGGAAGATCATACCTATTATTGGGAATTTGCCACAGACAGTATGACATTC 1094
Db 731 CCACCCATGAAGAAGATCATATCTCTTTGGGAATTTGCCACAGACAAATATGACATTC 790
QY 1095 GCTTTGGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGTGATGTCATGTCA 1154
Db 791 GCTTTGGGTTGATTTTGAATGGACAGACTCTCCAAACACTGCTGTGTCAGTGTCA 850
QY 1155 GTGAGTCCAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1214
Db 851 GTGAGTCCAGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
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QY 1215 AAAAGAACCCAAACAGCCCTCTGCTGGATGAGATGTGTACTCTGTGTACCGCGGAGCTGTC 1274
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QY 1275 ACGAGGAAGTATATGACGACGACCCACCATATCCACGGGAGGAGTCTATCTCCTCAAGT 1334
|||||
Db 971 ATGAGGAGGTGTATGCTGGCGACCCATCAATATCCAGGGAGAGAGTCTATCTCCTCAAGT 1030
|||||
QY 1335 TTGATAATTCCTACTCTCTGTGGAGTCCCAAGTCCCGTCTACTACAGAGTCTATTATACFA 1394
|||||
Db 1031 TTGACAACTCCTACTCTTTGTGGCGTCAAAATCACTCTACTACAGAGTCTATTATACFA 1090
|||||
QY 1395 GATAGAGCTGTGTTCCCAAGTCCGAGTCCAGGGTGTAGACAAACATGACGTTTAAATT 1454
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Db 1091 GATAAAATGTTGTTACAAAGTCTGGAGTCTAGGTTGGCGAGAGATGACATTTAAATT 1150
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RESULT 5
AF501319 18140 bp DNA linear ROD 06-MAY-2002
LOCUS
DEFINITION Mus musculus peripheral benzodiazepine receptor associated protein
ACCESSION AF501319
VERSION AF501319.1 GI:20453988
KEYWORDS
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 18140)
AUTHORS Liu, J. and Papadopoulos, V.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2002) Department of Cell Biology, Georgetown
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC
20007, USA

FEATURES
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/db_xref="taxon:10090"
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protein PAP7"
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/db_xref="GI:20453989"
/translation="MAAQLNVEQLVSLDGLTSPDSEERPGAEGAPQTTPPSAPGN
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LLNKCPLLSAVASHRTKEEKEKRAAEERQREERERLQKEEKEKREEDR
LRREEERREIEERLLEQKQKQIMALNSQTAVQFOYAAQYPCNGEQQILIRQ
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AKHTHSEKYLEVLAEEALENGKPSLPIAAPSMMTRPQIKDFEKIKRODSVI
TVRGEVTVRPVTHEEGSLFWFATDSYDIGFVPEWTDSPNAASVHVSESSDE
BEEBENVTCEKAKNANKPLLDIEIVPYRRDCHEEVYAGSHQYVGRGVYLLKFDNS
YSLWRSKSVYRVYTR"
BASE COUNT 4818 a 3784 c 4071 g 5445 t 22 others
ORIGIN

Query Match 19.7%; Score 287.2; DB 10; Length 18140;
Best Local Similarity 99.0%; Pred. No. 4.2e-62;
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 896 CCAAAAGACTCTTCCAGTGTATTCAGTCCATCGATGGACAAGACCACAAATCAA 955
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Db 15039 COTTTAGACTCTCTCCAGTGTATTCAGCTCCATCCATGTGGACAAGACCACAAATCAA 15098
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QY 956 GACTTTAAAGAGAAGATTCCGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAA 1015
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Db 15099 GACTTTAAAGAGAAGATTCCGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAA 15158
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QY 1016 GTCTGTCACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCC 1075
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Db 15159 GTCTGTCACCGTCCGAGTCCCGACTCATGAGGAAGGATCATACCTATTTTGGGAATTTGCC 15218
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QY 1076 ACAGACAGATTATGACATGGGTTTGGGTTTATTTGAATGACAGACTCTCCAAATGCT 1135
|||||
Db 15219 ACAGACAGATTATGACATGGGTTTGGGTTTATTTGAATGACAGACTCTCCAAATGCT 15278
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QY 1136 GCTGTCACTGTCTCATGTCTAGTCCAGTCCAGTGACGAGGAGGAGGAGGAAG 1187
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Db 15279 GCTGTCACTGTCTCATGTCTAGTCCAGTCCAGTGACGAGGAGGAGGAGGAAG 15330
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RESULT 6
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LOCUS
DEFINITION Mus musculus clone RP23-172B15, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC121292
VERSION AC121292.1 GI:20806432
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 63971)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP23-172B15
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 63971)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeAtrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severi, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zemlek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23476
Center clone name: 172_B_15
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* NOTE: This record contains 79 individual
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 717: contig of 717 bp in length
* 718 817: gap of 100 bp
* 818 1503: contig of 686 bp in length
* 1504 1603: gap of 100 bp
* 1604 2317: contig of 714 bp in length
* 2318 2417: gap of 100 bp
* 2418 3133: contig of 716 bp in length
* 3134 3233: gap of 100 bp
* 3234 3959: contig of 726 bp in length
* 3960 4059: gap of 100 bp
* 4060 4780: contig of 721 bp in length
* 4781 4880: gap of 100 bp
* 4881 5585: contig of 705 bp in length
* 5586 5685: gap of 100 bp
* 5686 6398: contig of 713 bp in length
* 6399 6498: gap of 100 bp
* 6499 7202: contig of 704 bp in length
* 7203 7302: gap of 100 bp
* 7303 8010: contig of 708 bp in length
* 8011 8110: gap of 100 bp
* 8111 8835: contig of 725 bp in length
* 8836 8935: gap of 100 bp
* 8936 9652: contig of 717 bp in length
* 9653 9752: gap of 100 bp
* 9753 10487: contig of 735 bp in length
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* 55160 55872: contig of 713 bp in length
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Query Match
Best Local Similarity 16.9%; Score 246.2; DB 2; Length 63971;
Matches 259; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1186 AGAAATGTCACCTGTGAAGAAAAGCAAAAGCAACGCGCAACGCCCTCTCTGGATGA 1245
DB 33662 AGAAATGTCACCTGTGAAGAAAAGCAAAAGCAACGCGCAACGCCCTCTCTGGATGA 33721

QY 1246 GATTGACCTGTGTACCGGC-GGGACTGTACAGGAAGATATATGAGCAGCCACCACGAT 1304
DB 33722 GATTGACCTGTGTACCGCGGGGAGTGTACAGGAAGATATATGAGCAGCCACCACGAT 33781

QY 1305 ATCCAGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGTGCCA 1364
DB 33782 ATCCAGGAGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGTGCCA 33841

QY 1365 AGTCCGCTACTACAGAGTCTATTATCTACTAGATAGAGCTGCTGTTCCAGGTCGCGGAGTC 1424
DB 33842 AGTCCGCTACTACAGAGTCTATTATCTACTAGATAGAGCTGCTGTTCCAGGTCGCGGAGTC 33901

QY 1425 CAGGTTGAGCAACATGACGT 1447
DB 33902 TAGGTTGAGCAACATGACGT 33924

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RESULT 7

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LOCUS          AC044825          140409 bp      DNA      linear      HTG 27-JUL-2000
DEFINITION    Homo sapiens chromosome 1 clone RP11-275114 map 1, WORKING DRAFT
SEQUENCE      AC044825
ACCESSION     AC044825.2  GI:9502452
VERSION       HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS      Homo sapiens.
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 140409)
AUTHORS       Birren,B., Linton,L., Nusbaum,C., Brown,A., Borkhater,B., Borkhater,B.,
              Boguslavsky,L., Boukhgaiter,B., Brown,A., Burkett,G.,
              Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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              Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
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              Young,G., Zainoun,J., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
SUBMITTED (12-APR-2000) Whitehead Institute/MIT Center for Genome
RESEARCH, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT       On Jul 27, 2000 this sequence version replaced gi:7543788.
              All repeats were identified using RepeatMasker:
              Smt, A.F.A. & Green, P. (1996-1997)
              http://ftp.genome.washington.edu/RM/RepeatMasker.html

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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 275_I_14
Center clone name: 18011
----- Summary Statistics
Sequencing vector: M13: W7815; 99% of reads
Sequencing vector: Plasmid; n/a; 0.0% of reads
1.00182149362477Chemistry: Dye-terminator Big Dye; 100% of
reads
Assembly program: Phrap; version 0.960731
Consensus quality: 120391 bases at least Q40
Consensus quality: 129577 bases at least Q30
Consensus quality: 133768 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 136609; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality co.
NOTE: This is a 'working draft' sequence. It currently
consists of 39 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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2366 3576: contig of 1211 bp in length
3577 3676: gap of 100 bp
3677 4845: contig of 1169 bp in length
4846 4945: gap of 100 bp
4946 7367: contig of 2422 bp in length
7368 7467: gap of 100 bp
7468 8595: contig of 1128 bp in length
8596 8695: gap of 100 bp
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10410 10509: gap of 100 bp
10510 11838: contig of 1329 bp in length
11839 11938: gap of 100 bp
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13893 15478: contig of 1586 bp in length
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* 22400 gap of unknown length
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Db 178929 CTTTGAAGATCTCTTCCAGTAATAGCAGCTCCATCCATGTCGACAGACCAACAA 178970

Qy 956 GACITTAAGAGAGATTCGGCAGGATCGAGATTCGTGATTACAGTAGTCGAGAGAA 1015
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Qy 1016 GPCGTCACCGTCGAGTCCCGACTCATGAGGAGATCATACCTATTTTGGGAATTTGCC 1075
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Db 178809 GTGGTCACTGTTTCGAGTACCCACCCATGAAGAGATCATATCTCTTTGGGAATTTGCC 178750

Qy 1076 ACAGACAGTTATGACATTTGGGTTTGGGTTTATTTTGAATGGACAGACTCTCCAATGCT 1135
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Db 178749 ACAGACAATTATGACATTTGGGTTTGGGTTGATTTTGAATGGACAGACTCTCCAACACT 178690

Qy 1136 GCTGTGAGTGTGATGTCAGTGAGTCCAGTACGAGGAGGAGGAGAGAGAAATGTC 1195
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Db 178689 GCTGTGAGTGTGATGTCAGTGAGTCCAGTACGAGGAGGAGGAGAGAGAGTGAACC 178630
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QY 1196 ACTGTGTGAAGAAAAGCA 1213
 Db 178629 CTGTGTCATATTCAGTA 178612
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 SOURCE Norway rat.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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 1 (bases 1 to 174143)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
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 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 174143)
 Worley,K.C.
 Title
 Submitted (05-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 174143)
 Worley,K.C.
 Title
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA
 On Jul 7, 2002 this sequence version replaced gi:21699099.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GIBG
 Center clone name: CH230-162N10
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 Sequencing vector: Plasmid:
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap: version 0.990329
 Consensus quality: 107819 bases at least Q40
 Consensus quality: 114791 bases at least Q30
 Consensus quality: 119520 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: this is a 'working draft' sequence. It currently
 consists of 70 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 as soon as it is available and the accession number will
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1 1306: contig of 1306 bp in length
 * 1307 1406: gap of unknown length
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 * 2497 2596: gap of unknown length
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VERSION AK095650.1 GI:21754954
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens fetal brain cDNA to mRNA, clone_lib.FCBBF3
clone:FCBBF3025285.

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1
Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoka,S.,
Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Watanabe,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A.,
Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K.,
Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3547)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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Evaluation; clone selection for full insert sequencing: HRI and
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RESULT 15
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DEFINITION Sequence 238 from Patent WO0218424.
ACCESSION AX400067
VERSION AX400067.1 GI:21336485
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1
Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J.,
Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
Nucleic acids and polypeptides
Patent: WO 0218424-A 238 07-MAR-2002;
HYSEQ, INC. (US)

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Query Match 10.3%; Score 150; DB 6; Length 882;
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Matches 304; Conservative 0; Mismatches 195; Indels 27; Gaps 1;

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Db 355 AAAGTCTCCACCTCTGATGGCTCTCCATCCATGCATCTGGACCTTTGCCAAGGTGAAGAA 414
Qy 959 TTAAAGAGAGATTCGGCAGGATGCAGATCTGTGATTACAGTACGTCGAGGAGAAATC 1018
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Qy 1139 GTCAGTGTGCATGTGTCAGTGTCCAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1193
Db 595 ATAAGTGTGCAGGTGTCAGTGTCCAGTGCAGGATGAGGATGAGGAGGAGGAGGAGG 654
Qy 1194 -----TCAGTTGTGAAGAAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
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Db 655 GAGATTGAAGAACCGTTCCAGCTGGAGATGTGGAGAGAGGCTCCAGGAGCTCCTTGCGG 714
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QY 1292 GGCAGCCACCATGATCCAGGGAGGGAGTCTATCTCCTCAAGTTTGATAAATTCCTACTCT 1351
Db 775 GGCAGCCATGACTACCTGTTGAGGGCATCTACCTGCTCAAGTTCGACAACCTCTACTCC 834
QY 1352 CTGTGGAGTCCAGTCCCTCTACTACAGAGTCTATTATAGAT 1397
Db 835 CTGTGGCAACAGACTCTCTACTTCCACATCTACTACACAGCT 880

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